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caaaaacagc a gcaccaacc at Me 1	eg goo acg ttt gtg gag oto agt aco aaa goo aag atg coo et Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro 5 10	111
caaaaacagc a gcaccaacc at Me 1 att gtg ggc	cg gcc acg ttt gtg gag ctc agt acc aaa gcc aag atg ccc et Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro 5 10  ctg ggc act tgg aag tct cct ctc ggc aaa gtg aaa gaa	
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caaaaacagc a gcaccaacc at Me 1 att gtg ggc Ile Val Gly	cg gcc acg ttt gtg gag ctc agt acc aaa gcc aag atg ccc et Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro 5 10  ctg ggc act tgg aag tct cct ctc ggc aaa gtg aaa gaa Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu 20 25 30	111 159
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caaaaacagc a gcaccaacc at Me 1 att gtg ggc Ile Val Gly 15 gca gtg aag	ctg gcc acg ttt gtg gag ctc agt acc aaa gcc aag atg ccc et Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro 5 10  ctg ggc act tgg aag tct cct ctc ggc aaa gtg aaa gaa Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu 20 25 30  gtg gcc att gat gca gga tat cgg cac att gac tgt gcc Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala	111 159
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caaaaacagc a gcaccaacc at Me 1 att gtg ggc Ile Val Gly 15 gca gtg aag Ala Val Lys tat gtc tat of Tyr Val Tyr atc caa gag Ile Gln Glu I 65	Eg gcc acg ttt gtg gag ctc agt acc aaa gcc aag atg ccc at Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro 5 10  Ctg ggc act tgg aag tct cct ctc ggc aaa gtg aaa gaa Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu 20 25 30  gtg gcc att gat gca gga tat cgg cac att gac tgt gcc Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala 35 40 45  cag aat gaa cat gaa gtg ggg gaa gcc atc caa gag aag Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys 50 55 60  aag gct gtg aag cgg gag gac ctg ttc atc gtc agc aag Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys 70 75	111 159 207 255
caaaaacagc ac gcaccaacc at Me  1  att gtg ggc Ile Val Gly Is  gca gtg aag GAla Val Lys  tat gtc tat GTyr Val Tyr Galaccaa gag alle Gln Glu I G5  ttg tgg ccc ac gcaccaccaccaccaccaccaccaccaccaccaccaccac	The second secon	111 159 207 255
caaaaacagc ac gcaccaacc at Me  1  att gtg ggc Ile Val Gly Is  gca gtg aag GAla Val Lys  tat gtc tat GTyr Val Tyr Galaccaa gag alle Gln Glu I G5  ttg tgg ccc ac gcaccaccaccaccaccaccaccaccaccaccaccaccac	Eg gcc acg ttt gtg gag ctc agt acc aaa gcc aag atg ccc at Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro 5 10  Ctg ggc act tgg aag tct cct ctc ggc aaa gtg aaa gaa Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu 20 25 30  gtg gcc att gat gca gga tat cgg cac att gac tgt gcc Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala 35 40 45  cag aat gaa cat gaa gtg ggg gaa gcc atc caa gag aag Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys 50 55 60  aag gct gtg aag cgg gag gac ctg ttc atc gtc agc aag Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys 70 75	111 159 207 255

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<211> .88

<212> PRT

<213> ARTIFICIAL SEQUENCE

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Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu Ala Val
20 25 30

Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala Tyr Val 35 40 45

Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys Ile Gln 50 55 60

Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys Leu Trp

65 70 75 80

Pro Thr Ser Arg Ser Arg Ser Ser 85

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att gtg ggc ctg ggc act tgg aag tct cct ctc ggc aaa gtg aaa gaa Ile Val Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu 15 20 25 30	159
gca gtg aag gtg gcc att gat gca gga tat cgg cac att gac tgt gcc Ala Val Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala 35 40 45	207
tat gtc tat cag aat gaa cat gaa gtg ggg gaa gcc atc caa gag aag Tyr Val Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys 50 55 60	255
atc caa gag aag gct gtg aag cgg gag gac ctg ttc atc gtc agc aag Ile Gln Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys 65 70 75	303
ttg tgg ccc act ttc ttt gag aga ccc ctt gtg agg aaa gcc ttt gag Leu Trp Pro Thr Phe Phe Glu Arg Pro Leu Val Arg Lys Ala Phe Glu 80 85 90	351
aag acc ctc aag gac ctg aag ctg agc tat ctg gac gtc tat ctt att Lys Thr Leu Lys Asp Leu Lys Leu Ser Tyr Leu Asp Val Tyr Leu Ile 95 100 105 110	399
cac tgg cca cag gga ttc aag tct ggg gat gac ctt ttc ccc aaa gat His Trp Pro Gln Gly Phe Lys Ser Gly Asp Asp Leu Phe Pro Lys Asp 115 120 125	447

gat a Asp L																495
gag g Glu A	Ala															543
gtc t Val S 1							_									591
gga c Gly L 175																639
ctc a	-	_			_		_		_							687
gtt a		Ala		-		-			_							735
cca g	lu i															783
gca aa Ala Ly 24	_				_	_	tgac	acca	.gc a	ıcgca	ttgt	t ga	igaad	atto	:	834
aggtct	tttg	ga c	ttta	aatt	g ag	tgat	gagg	aga	tggc	aac	cata	ctca	igc t	tcaa	cagaa	894
actgga	aggg	gc c	tgta	acgt	g tt	gcaa	tcct	ctc	attt	gga	agac	tato	cc t	tcga	tgcag	954
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atctga	atca	ag a	acaa	atgt	t ta	ttaa	gcat	cag	aaac	tct	gcca	acac	tg a	ggat	gtaaa	1254
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<210> 4

<211> 245

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

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<223> PEPTIDE ENCODED BY VARIANT OF HUMAN ALDOSE REDUCTASE-LIKE GENE

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Met Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro Ile Val 1 5 10 15

Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu Ala Val 20 25 30

Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala Tyr Val 35 40 45

Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys Ile Gln 50 55 60

Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys Leu Trp 65 70 75 80

Pro Thr Phe Phe Glu Arg Pro Leu Val Arg Lys Ala Phe Glu Lys Thr 85 90 95

Leu Lys Asp Leu Lys Leu Ser Tyr Leu Asp Val Tyr Leu Ile His Trp
100 105 110

Pro Gln Gly Phe Lys Ser Gly Asp Asp Leu Phe Pro Lys Asp Asp Lys
115 120 125

Gly Asn Ala Ile Gly Gly Lys Ala Thr Phe Leu Asp Ala Trp Glu Ala 130 135 140

Met Glu Glu Leu Val Asp Glu Gly Leu Val Lys Ala Leu Gly Val Ser 145 150 155 160

Asn Phe Ser His Phe Gln Ile Glu Lys Leu Leu Asn Lys Pro Gly Leu 165 170 175

Lys Tyr Lys Pro Val Thr Asn Gln Val Glu Cys His Pro Tyr Leu Thr
180 185 190

Gln Glu Lys Leu Ile Gln Tyr Cys His Ser Lys Gly Ile Thr Val Thr

195 200 205

Ala Tyr Ser Pro Leu Gly Ser Pro Asp Arg Pro Trp Ala Lys Pro Glu 210 215 220

Asp Pro Ser Leu Leu Glu Asp Pro Lys Ile Lys Glu Ile Ala Ala Lys 225 230 235 240

His Ser Pro Ser Leu 245

<210> 5

<211> 1337

<212> DNA

<213> HOMO SAPIEN

<220>

<223> HUMAN ARL GENE

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gccatccaag	agaagatcca	agagaaggct	gtgaagcggg	aggacctgtt	catcgtcagc	300
aagttgtggc	ccactttctt	tgagagaccc	cttgtgagga	aagcctttga	gaagaccctc	360
aaggacctga	agctgagcta	tctggacgtc	tatcttattc	actggccaca	gggattcaag	420
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<210> 6

- <211> 316
- <212> PRT
- <213> HOMO SAPIEN
- <220>
- <223> AMINO ACID SEQUENCE ENCODED BY HUMAN ARL GENE
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- Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu Ala Val 20 25 30
- Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala Tyr Val 35 40 45
- Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys Ile Gln 50 55 60
- Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys Leu Trp 65 70 75 80
- Pro Thr Phe Phe Glu Arg Pro Leu Val Arg Lys Ala Phe Glu Lys Thr 85 90 95
- Leu Lys Asp Leu Lys Leu Ser Tyr Leu Asp Val Tyr Leu Ile His Trp
  100 105 110
- Pro Gln Gly Phe Lys Ser Gly Asp Asp Leu Phe Pro Lys Asp Asp Lys 115 120 125
- Gly Asn Ala Ile Gly Gly Lys Ala Thr Phe Leu Asp Ala Trp Glu Ala 130 135 140
- Met Glu Glu Leu Val Asp Glu Gly Leu Val Lys Ala Leu Gly Val Ser 145 150 155 160
- Asn Phe Ser His Phe Gln Ile Glu Lys Leu Leu Asn Lys Pro Gly Leu 165 170 175
- Lys Tyr Lys Pro Val Thr Asn Gln Val Glu Cys His Pro Tyr Leu Thr 180 185 190
- Gln Glu Lys Leu Ile Gln Tyr Cys His Ser Lys Gly Ile Thr Val Thr 195 200 205
- Ala Tyr Ser Pro Leu Gly Ser Pro Asp Arg Pro Trp Ala Lys Pro Glu 210 215 220

Asp Pro Ser Leu Leu Glu Asp Pro Lys Ile Lys Glu Ile Ala Ala Lys 225 230 235 240

His Lys Lys Thr Ala Ala Gln Val Leu Ile Arg Phe His Ile Gln Arg 245 250 255

Asn Val Ile Val Ile Pro Lys Ser Val Thr Pro Ala Arg Ile Val Glu 260 265 270

Asn Ile Gln Val Phe Asp Phe Lys Leu Ser Asp Glu Glu Met Ala Thr 275 280 285

Ile Leu Ser Phe Asn Arg Asn Trp Arg Ala Cys Asn Val Leu Gln Ser 290 295 300

Ser His Leu Glu Asp Tyr Pro Phe Asp Ala Glu Tyr 305 310 315